

BLAST! 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query: seq6
(252 letters)

Database: blastrge.txt
7 sequences; 13,979 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gb AF016295.1 AF016295 Homo sapiens Ets transcription factor (EL...	500	e-144
gb AR020776.1 AR020776 Sequence 1 from patent US 5789200	500	e-144
gb U97156.1 HSU97156 Homo sapiens epithelial-specific ets protei...	500	e-144
gb U73843.1 HSU73843 Homo sapiens epithelial-specific transcript...	500	e-144
gb AF017307.1 AF017307 Homo sapiens Ets-related transcription fa...	500	e-144
gb U66894.1 HSU66894 Human epithelium-restricted Ets protein ESX...	500	e-144
gb U73844.1 HSU73844 Homo sapiens epithelial-specific transcript...	412	e-118

>gb|AF016295.1|AF016295 Homo sapiens Ets transcription factor (ELF3) mRNA,
complete cds
Length = 1920

Score = 500 bits (252), Expect = e-144
Identities = 252/252 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 60
|||||
Sbjct: 424 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 483

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
|||||
Sbjct: 484 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 543

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 180
|||||
Sbjct: 544 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 603

Query: 181 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
|||||
Sbjct: 604 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 663

Query: 241 tgtggcgagga 252

|||||
Sbjct: 664 tgtggcgagga 675

>gb|AR020776.1|AR020776 Sequence 1 from patent US 5789200
Length = 1920

Score = 500 bits (252), Expect = e-144
Identities = 252/252 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 60
|||||
Sbjct: 424 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 483

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
|||||
Sbjct: 484 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 543

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 180
|||||
Sbjct: 544 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 603

Query: 181 ccctttgccagagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
|||||
Sbjct: 604 ccctttgccagagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 663

Query: 241 tgtggcgagga 252
|||||
Sbjct: 664 tgtggcgagga 675

>gb|U97156.1|HSU97156 Homo sapiens epithelial-specific ets protein (jen) mRNA,
complete
cds
Length = 1942

Score = 500 bits (252), Expect = e-144
Identities = 252/252 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 60
|||||
Sbjct: 434 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 493

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
|||||
Sbjct: 494 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 553

Query: 121 gagaaggatggcatggccttccaggaggccctagacccagggccctttgaccagggcagc 180
|||||
Sbjct: 554 gagaaggatggcatggccttccaggaggccctagacccagggccctttgaccagggcagc 613

Query: 181 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
|||||
Sbjct: 614 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 673

Query: 241 tgtggcgagga 252
|||||
Sbjct: 674 tgtggcgagga 685

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 231 ccccgagcagct 241
|||||
Sbjct: 694 ccccgagcagct 704

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 144 ggaggccctag 154
|||||
Sbjct: 1587 ggaggccctag 1597

>gb|U73843.1|HSU73843 Homo sapiens epithelial-specific transcription factor ESE-
1b
(ESE-1) mRNA, complete cds
Length = 1915

Score = 500 bits (252), Expect = e-144
Identities = 252/252 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 60
|||||
Sbjct: 429 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 488

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
|||||
Sbjct: 489 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 548

Query: 121 gagaaggatggcatggccttccaggaggccctagacccagggccctttgaccagggcagc 180
|||||

Sbjct: 549 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 608

Query: 181 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
|||||

Sbjct: 609 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 668

Query: 241 tgtggcgagga 252
|||||

Sbjct: 669 tgtggcgagga 680

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 144 ggaggccctag 154
|||||

Sbjct: 1583 ggaggccctag 1593

>gb|AF017307.1|AF017307 Homo sapiens Ets-related transcription factor (ERT)
mRNA, complete
cds
Length = 2529

Score = 500 bits (252), Expect = e-144
Identities = 252/252 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgctctggtctttgggcctctgggggaccaactccatgcc 60
|||||

Sbjct: 512 aattgtgcccttgaggagctgcgctctggtctttgggcctctgggggaccaactccatgcc 571

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
|||||

Sbjct: 572 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 631

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 180
|||||

Sbjct: 632 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 691

Query: 181 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
|||||

Sbjct: 692 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 751

Query: 241 tgtggcgagga 252
|||||

Sbjct: 752 tgtggcgagga 763

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 231 ccccggcagct 241
 |||||
Sbjct: 772 ccccggcagct 782

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 144 ggaggccctag 154
 |||||
Sbjct: 1665 ggaggccctag 1675

>gb|U66894.1|HSU66894 Human epithelium-restricted Ets protein ESX mRNA, complete
cds

Length = 1907

Score = 500 bits (252), Expect = e-144
Identities = 252/252 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctggtccttgggcctctgggggaccaactccatgcc 60
 |||||
Sbjct: 405 aattgtgcccttgaggagctgcgtctggtccttgggcctctgggggaccaactccatgcc 464

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
 |||||
Sbjct: 465 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 524

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 180
 |||||
Sbjct: 525 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 584

Query: 181 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
 |||||
Sbjct: 585 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 644

Query: 241 tgtggcgagga 252
 |||||
Sbjct: 645 tgtggcgagga 656

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)

Strand = Plus / Plus

Query: 144 ggaggccctag 154
|||||||
Sbjct: 1559 ggaggccctag 1569

>gb|U73844.1|HSU73844 Homo sapiens epithelial-specific transcription factor ESE-1a

(ESE-1) mRNA, complete cds
Length = 1846

Score = 412 bits (208), Expect = e-118
Identities = 208/208 (100%)
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgCGTCTGGTCTTTGGGCCTCTGGGGGACCAACTCCATGCC 60
|||||||
Sbjct: 429 aattgtgcccttgaggagctgCGTCTGGTCTTTGGGCCTCTGGGGGACCAACTCCATGCC 488

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
|||||||
Sbjct: 489 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 548

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 180
|||||||
Sbjct: 549 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 608

Query: 181 ccctttgcccaggagctgctggacgacg 208
|||||||
Sbjct: 609 ccctttgcccaggagctgctggacgacg 636

Score = 22.3 bits (11), Expect = 0.65
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 144 ggaggccctag 154
|||||||
Sbjct: 1514 ggaggccctag 1524

Database: blastrge.txt

Posted date: Nov 30, 1999 9:59 AM
Number of letters in database: 13,979
Number of sequences in database: 7

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 28
Number of Sequences: 7
Number of extensions: 28
Number of successful extensions: 28
Number of sequences better than 10.0: 7
length of query: 252
length of database: 13,979
effective HSP length: 11
effective length of query: 241
effective length of database: 13,902
effective search space: 3350382
effective search space used: 3350382
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 25 (49.6 bits)
S1: 12 (24.3 bits)
S2: 10 (20.3 bits)